AMENDMENTS TO THE CLAIMS:

Pursuant to 37 C.F.R. § 1.121, please amend the claims as follows. The following listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

The following listing of claims replaces all prior versions and listings of claims in the application.

1. (Currently Amended) An isolated or recombinant ~~A~~ Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide variant comprising ~~having~~ an amino acid sequence ~~comprising~~ which differs from the amino acid sequence of ~~1-15 amino acid modifications relative to~~ human Factor VII (hFVII) or human Factor VIIa (hFVIIa) ~~having the amino acid sequence~~ shown in SEQ ID NO:1 in no more than 15 amino acid residues, wherein the leucine (L) in position 65 of SEQ ID NO:1 is substituted with a glutamine (Q) in said variant sequence, and wherein amino acid positions of the variant sequence are numbered according to SEQ ID NO:1 ~~comprises a substitution in at least one position selected from the group consisting of L39, I42, S43, K62, L65, F71, E82 and F275,~~

~~with the proviso that said variant is not~~

~~[K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[I42N]hFVII/hFVIIa or [I42S]hFVII/hFVIIa or [I42A]hFVII/hFVIIa or [I42Q]hFVII/hFVIIa~~.

2. (Currently Amended) The variant according to claim 1, wherein said variant sequence further comprises at least one amino acid substitution selected from the group consisting of L39E, L39Q, L39H, I42R, S43H, S43Q, K62E, K62R, ~~L65Q,~~ L65S, F71D, F71Y, F71E, F71Q, F71N, E82Q, E82N, E82K and F275H~~,~~

~~with the proviso that said variant is not~~

~~[K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A1Y+A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [A3S+F4GK+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or~~

~~[A3S+F4GK+L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa or [L8F+R9V+P10Q+K32E+D33N+A34T+K38T+L39E]hFVII/hFVIIa~~.

3-6. (Cancelled)

7. (Currently Amended) The variant according to claim 2 ~~1~~, wherein said ~~variant comprises~~ at least one amino acid substitution is ~~two substitutions selected from the group consisting of L65Q,~~ F71Y, K62E or ~~and~~ S43Q.

8-12. (Cancelled)

13. (Currently Amended) The variant according to claim 1, wherein said variant further comprises at least one amino acid substitution ~~modification~~ in the Gla domain.

14. (Currently Amended) The variant according to claim 13, wherein said at least one amino acid substitution ~~modification~~ in the Gla domain ~~comprises a substitution in at least one position~~ is selected from the group consisting of P10, K32, D33 and A34.

15-24. (Cancelled)

25. (Currently Amended) The variant according to claim 1, wherein an ~~at least one~~ amino acid residue comprising an attachment group for a non-polypeptide moiety has been introduced in the variant sequence in a position located outside the Gla domain.

26. (Currently Amended) The variant according to claim 25, wherein the ~~at least one~~ non-polypeptide moiety is covalently attached to the ~~at least one of said~~ attachment group ~~groups~~.

27. (Original) The variant according to claim 26, wherein said non-polypeptide moiety is a sugar moiety.

28. (Previously Presented) The variant according to claim 25, wherein said attachment group is a glycosylation site.

29. (Cancelled)

30. (Currently Amended) The variant according to claim 28, wherein said glycosylation site is introduced by amino acid substitution ~~and said introduced glycosylation site is an *in vivo* glycosylation site~~.

31. (Cancelled)

32. (Currently Amended) The variant according to claim 30, wherein said introduced ~~*in vivo*~~ glycosylation site is an N-glycosylation site.

33-34. (Cancelled)

35. (Previously Presented) The variant according to claim 32, wherein said N-glycosylation site is introduced by a substitution selected from the group consisting of A51N, G58N, G48N+S60T, T106N, K109N, G124N, K143N+N145T, A175T, I205S, I205T, V253N, T267N, T267N+S269T, S314N+K316S, S314N+K316T, R315N+V317S, R315N+V317T, K316N+G318S, K316N+G318T, G318N, and D334N.

36-49. (Cancelled)

50. (Previously Presented) The variant according to claim 1, wherein said variant is in its activated form.

51. (Withdrawn) A nucleotide sequence encoding the variant according to claim 1.

52. (Cancelled)

53. (Withdrawn) A host cell comprising the nucleotide sequence according to claim 51.

54. (Withdrawn) The host cell according to claim 53, wherein said host cell is a gammacarboxylating cell capable of *in vivo* glycosylation.

55. (Currently Amended) A pharmaceutical composition comprising the variant according to claim 1, and a pharmaceutically ~~pharmaceutical~~ acceptable carrier or excipient.

56-61. (Cancelled)

62. (Withdrawn) A method for treating a mammal having a disease or a disorder wherein clot formation is desirable, comprising administering to a mammal in need thereof an effective amount of the pharmaceutical composition according to claim 55.

63. (Withdrawn – Currently Amended) The method according to claim 62, wherein said disease or disorder is selected ~~**selcted**~~ from the group consisting of hemorrhage~~**,;**~~ uncontrolled ~~**bleedings**~~ bleeding, ~~**such as trauma;**~~ cirrhosis~~**,;**~~ thrombocytopenia~~**,;**~~ and hemophilia ~~**haemophilia A and haemophilia B**~~.

64-66. (Cancelled)